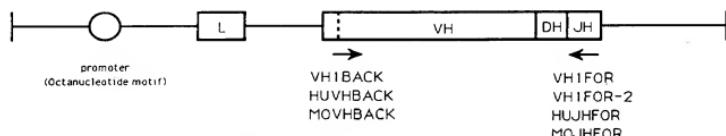




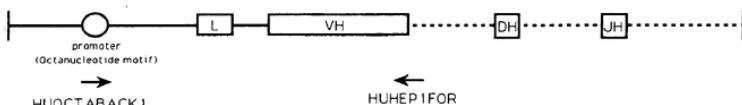
Inventor: Gregory P. WINTER,
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6545142

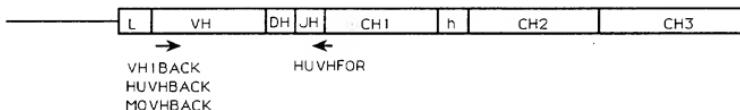
Rearranged heavy chain variable gene (DNA)



Unrearranged heavy chain variable gene (DNA)



Rearranged heavy chain variable gene (mRNA)



Rearranged light chain variable gene (DNA)

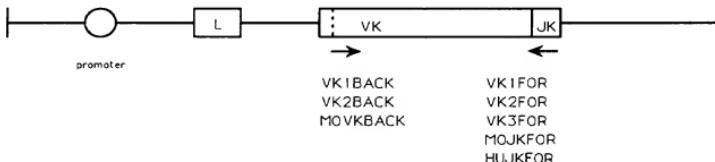


FIG. 1



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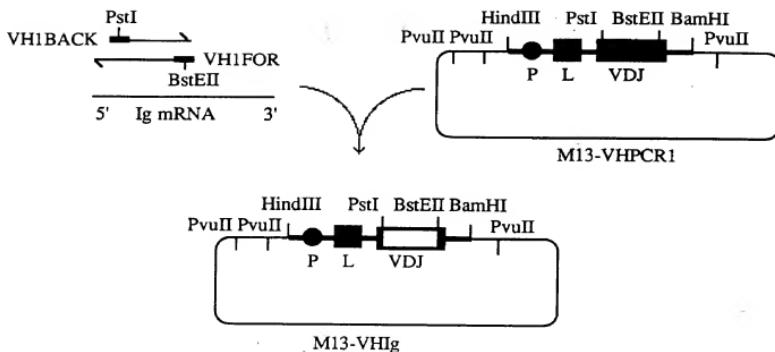


FIG. 2

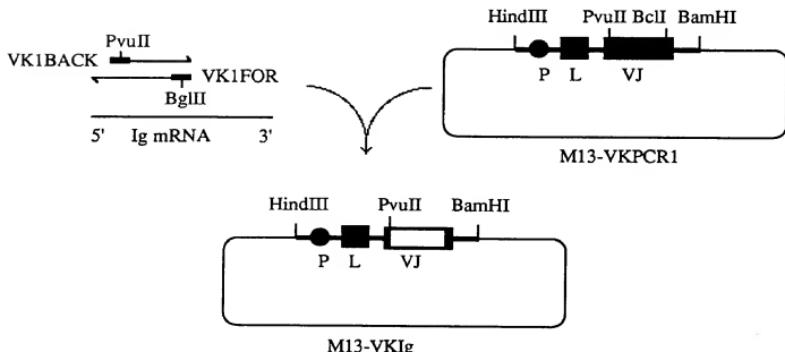


FIG. 4



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M13 VHPCR1

HinD III⁽¹⁾

AAGCTTATGAATATGCAAATCCTCTGAATCTACATGGTAAATATAGGTTGTCTATACCA
 10 20 30 40 50 60
 CAAACAGAAAAACATGAGATCACAGTTCTCTACAGTTACTGAGCACACAGGACCTCAC
 70 80 90 100 110 120

M G W S C I I L F L V A T A T
 CATGGGATGGAGCTGTATCCTCTTCTGGTACAGCTACAGGTAAGGGCTCAC
 130 140 150 160 170 180

AGTAGCAGGCTTGAGGCTGGACATATATGGGTGACAATGACATCCACTTGCCCTTC
 190 200 210 220 230 240

PstI
 G V H S Q V Q L Q E S G P G L V R P
 1 51 10
 TCTCCACAGGTGTCACCTCCAGGTCACACTGCAGAGAGCGGTCCAGGTCTGTGAGAC
 250 260 270 280 290 300

CDR1
 S Q T L S L T C T V S G S T F S S Y W M
 CTAGCCAGACCTGAGCTGACCTGACCCGTGCTGGCAGCACCTTCAGCAGCTACTGGA
 310 320 330 340 350 360

CDR2
 15 20 25 30
 H W V R Q P P G R G L E W I G R I D P N
 TGCACTGGGTGAGACAGCCACCTGGACAGGGCTCTGGAGTGGATTGGAGGATTGATCTTA
 370 380 390 400 410 420

35 40 45 50
 S G G T K Y N E K F K S R V T M L V D T
 ATAGTGGTGTACTAACATGAGAAGTTCAAGACAGAGTGCACATGCTGGTAGACA
 430 440 450 460 470 480

55 60 65 70
 S K N Q F S L R L S S V T A A D T A V Y
 CCAGCAAGAACCGATTGACGGCTGAGACTCAGCAGCGTGACAGCCGCCACACCGCGGTCT
 490 500 510 520 530 540

CDR3
 95 100 105 110
 Y C A R Y D Y Y G S S Y F D Y W G Q G T
 ATTATTGTGCAAGATACTGATTACTACCGTAGCTACTTGTACTTGACTACTGAGCTTAAAT
 550 560 570 580 590 600

BstEII
 115 I 120
 T V T V S S
 CCACGGTCACCGTCTCCCTCAGGTGAGTCCCTACACCTCTCTCTTCTATTAGCTTAAAT
 610 620 630 640 650 660

AGATTTTACTGCATTTGGTGGGGGGAAATGTGTATCTGAATTTCAGGTATGAAGGA
 670 680 690 700 710 720

CTAGGGACACCTTGGAGTCAGAAAGGGTCATTGGGAGCCGGGCTATGCAAGACAGACA
 730 740 750 760 770 780

BamHI
 |
 TCCTCAGCTCCCGACTTCATGGCCAGAGATTATAG
 790 800 810

FIG. 3



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M13 V_kPCR1

Hind III

AAGCTTATGAAATATGCAAATCCTCTGAATCTACATGGTAAATATAGGTTGTCTATACCA
38 48 58 68 78 88

CAAACAGAAAAACATGAGATCACAGTTCTCTACAGTTACTGAGCACACAGGACCTCAC
98 108 118 128 138 148

M G W S C I I L F L V A T A T
CATGGGATGGAGCTGTATCATCCTCTTCTGGTACAGACAGCTACAGGTAAGGGGCTCAC
158 168 178 188 198 208

AGTAGCAGGCTTGGGTCTGGACATATATGGGTGACAATGACATCCACTTGCCTTTC
218 228 238 248 258 268

Pvu II

1 5 10
G V H S D I Q L T Q S P S S L S A S
TCTCCACAGGTGTCCACTCCGACATCCAGCTGACCCAGGCCAAGCAGCCCTGAGGCCA
278 288 298 308 318 328

CDR1

15 20 25 30
V G D R V T I T C R A S G N I H N Y L A
GCGTGGGTGACAGAGTGACCATCACCTGTAGAGCCAGCGGTAAACATCCACAACACTACCTGG
338 348 358 368 378 388

CDR2

35 40 45 50 55
W Y Q Q K P G K A P K L L I Y Y T T T L
CTTGGTACAGCAGAAGCCAGGTAAAGGTCCAAAGCTGCTGATCTACTACACCACCC
398 408 418 428 438 448

55 60 65 70
A D G V P S R F S G S G S G T D F T F T
TGGCTGACGGTGTGCCAACAGATTCAAGCGGTAGCGGTAGCGGTACCGACTTCACCTTC
458 468 478 488 498 508

CDR3

75 80 85 90
I S S L Q P E D I A T Y Y C Q H F W S T
CCATCAGCACGCCCTCAGGCCAGAGACATCGCCACCTACTGCCAGCACTTCTGGAGCA
518 528 538 548 558 568

Bcl I (requires dam⁻ host)

95 100 105 108
P R T F G Q G T K V V I K R
CCCCAAGGGACAGTCGGCCAGGGACCAAGGTGGTGTCAACCGTAGTAGAATTAAACT
578 588 598 608 618 628

BamHI

TTGCTTCCCTCAGTTGGATCC
638 648

FIG. 5



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Sequence of MBrl VH

Splice -1
 ↓ G V H S
 AGGTGTCCACTCC

1 PstI 10 20
 Q V Q L Q E S G T E L A S P G A S V T L
CAGGTCCAACTGCAGGAGTCAGGAACTGGCTGAGCTGGCGAGTCCTGGGGCATCAGTGACACTG
VH1BACK SITE

30 CDR1 40
 S C K A S' G Y T F T D H I I N W V K K R
TCCTGCAAGGCTTCTGGCTACACATTACTGACCATATAAATTGGGTAAAAAGAGG

52a 53 CDR2 52a 53
 P G Q G L E W I G R I Y P V S G V T N Y
CTCTGGACAGGCCCTTGAGTGGATGGAGGGATTATCAGTAAGTGGTGAACTAAC
 60 CDR2 65 70
 N O K F M G K A T F S V D R S S N T V Y
AATCAAAAATTATGGCGAAGGCCACATTCTCTGTAGACCGGTCTCCAACACAGTGAC
 80 82A B C 83 90 CDR3
 M V L N S L T S E D P A V Y Y C G R G F
ATGGTGTGACAGCTGACATCTGAGGACCTGTGTCTATTACTGTGGAAAGGGCTT
 CDR3 103 BstEII Splice
D F D Y W G Q G T T V T V S S ↓
GATTTGACTACTGGGCCAAGGGACCAACGGTCACCGTCTCCAGGT.....
VH1FOR SITE

Sequence of MBrl VK

Splice -1
 ↓ G V H S
 AGGTGTCCACTCC

1 PvuII 10 20
 D I Q L T Q S P P S L T V S V G E R V T
GACATTCAAGCTGACCCAGTCTCCACCATCCCTGACTGTGTAGTAGGAGAGAGGGTCACT
VH1BACK SITE

27A B C D E F CDR1
 I S C K S N O N L L W S G N R R Y C L G
ATCAGTTGCAAATCCATCAGAAATCTTTATGGAGTGGAAACCGAAGGTACTGTTGGC
 35 40 50 CDR2
 W H Q W K P G Q T P T P L I T W T S D R
TGGCACCAAGTGGAAACCAAGGCAAACCTCCATACCGTTGATCACCTGGACATCTGTAGAGG
 60 60 70
[F S] G V P D R F I G S G S V T D F T L T
TTCTCTGGAGTCCCTGATGCTTCAAGGCACTGTGACAGATTCACTGTGACCC
 80 80 90 CDR3
 I S S V Q A E D V A V Y F C Q Q H L D E
ATCAGCAGTGTGCGAGGTGAAGATGTGGCAGTTATTCTGTGACCAACATTGGACCTT
 95 100 BglII/BclI Splice
[P Y T] F G G T K L E I K ↓
CCGTACACGTTCGGGAGGGGACCAAGCTGGAGATCAAACGTGAG
VK1FOR SITE

FIG. 6



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α -Lys 30

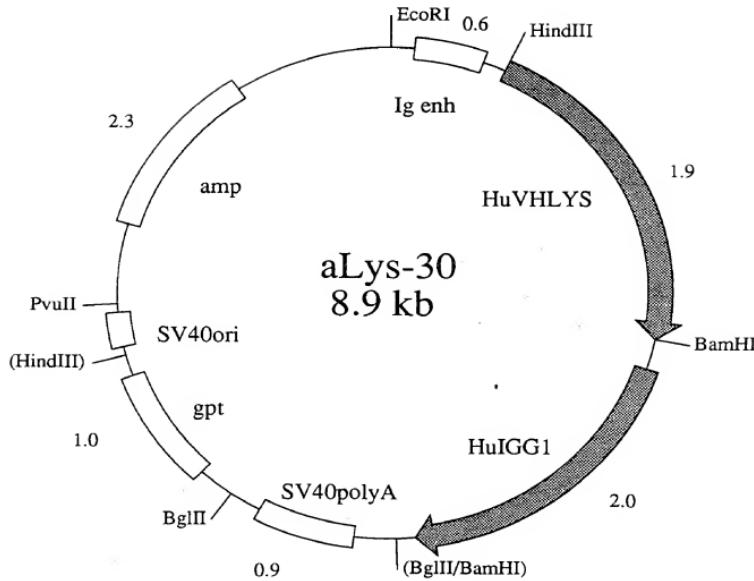


FIG. 7



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α -Lys 17

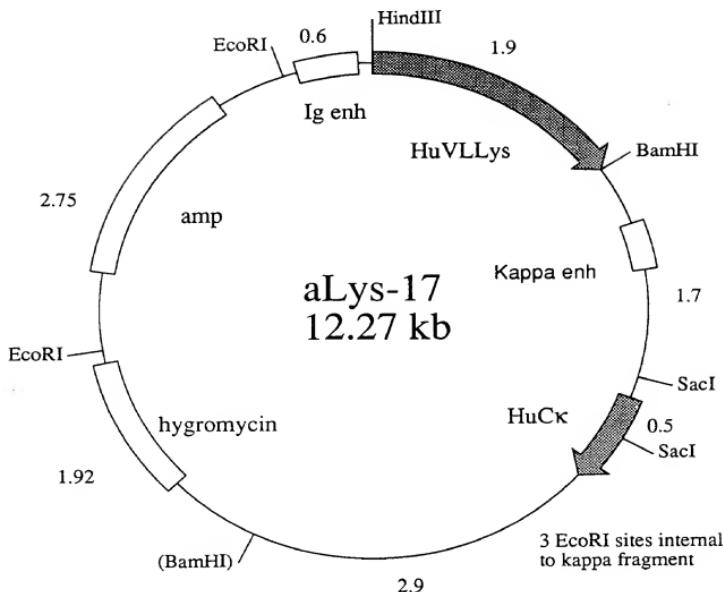


FIG. 8

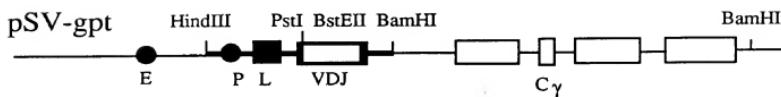
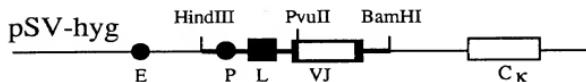


FIG. 9





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ER1

CDR 1

ER2

CDR 2

KABAT IA

A07	PGLVKPSQSLSLTCSVTGYSIT	SGYWN	WIRQFPGNKLEWMG	YISYDGSNNYNPSLKN
A09	PGLVKPSQSLFLTCSITGFPIT	SGYWN	WIRQSPGKLEWMG	YITHSGSETYNPNSLOS
E03	PGLVKPSQSLSLTCSVTGYSIT	SGYWN	WIRQFPGNKLEWMG	YISYDGSNNYNPSLKN
G01	PGLVKPSQSLSLTCSVTGYSIT	SGYWN	WIRQFPGNKLEWMG	YISYDGSNNYNPSLKN

KABAT IB

A06	PVLVAPSQSLSLTCAVSDFSLT	NYGV	WVRQPPGKCLEWLG	VIWAGGITNNSALMS
25C07	PGLVQPSQSLSLTCAVSDFSLT	SYGVH	WVRQSPGKLEWLG	VIWGGSTDNYNAAFIS
B03	PGLVQPSQSLSLTCAVSDFSLT	SYGVD	WVRQPPGKCLEWLG	VIWGGSTDNYNSALMS
G03	PGLVQPSQSLSLTCAVSDFSLT	SYGVH	WVRQSPGKCLEWLG	VIWGGSTDNYNAAFIS
H09	PVLVAPPQSLSLTCAVSDFSLT	SYGVH	WVRQPPGKCLEWLG	VIWAGGITNNSALMS
25C10	PGLVAPPQSLSLTCAVSDFSLT	SYAIS	WVRQPPGKCLEWLG	VIWAGGITNNSALMS
A1A	PGLVAPPQSLSLTCAVSDFSLT	SYAIS	WVRQPPGKCLEWLG	VIWAGGITNNSALMS
A08	PGLVAPPQSLSLTCAVSDFSLT	SYGVH	WVRQPPGKCLEWLW**	***GSTTINYNSALKS
25G08	PGLVAPPQSLSLTCAVSDFSLT	SYDWD	WVRQSPGKLEWLG	VIWGGSTDNYNSALMS
A03	PGLVAPPQSLSLTCAVSDFSLT	SYGVH	WVRQSPGKLEWLG	VIWGGSTDNYNAAFIS
C07	PGLVAPPQSLSLTCAVSDFSLT	SYGVH	WVRQSPGKLEWLG	VIWAGGITNNSALMS
H04	PGLVAPPQSLSLTCAVSDFSLT	SYGVD	WVRQSPGKLEWLG	VIWVGSTDNYNSALKS

KABAT IIA

E04	PELVRPGVSVKISCKGSGYIFT	DYAMH	WVKQSHAKSLEWIG	VISTYYGDASYNQKFKD
H07	PELVRPGVSVKISCKGSGYIFT	DYAMH	WVKQSHAKSLEWIG	VISTYYGDASYNQKFKD

KABAT IIB

A02	AELVMPGASVKLSCASGYIFT	SYWMH	WVKQRPQGQLEWIG	EIDPSDSYTINYNQKFKG
B04	AELVRPQGASVKMSCKASGYIFT	SYWIT	WVKQRPQGQLEWIG	DIYPSGSSTINYNEKFKS
C05	AELVRPQGASVKLSCASGYIFT	SYWMH	WVKQRPGRGLEWIG	RIDPNSGGTINYNEKFKS
C09	AELVRPQGASVKLSCASGYIFT	SYWMH	WVKQRPQGQLEWIG	EINPNSGGTINYDEKFKS
D06	ASLVRPQGASVKMSCKASGYIFT	SYWIT	WVKQRPQGQLEWIG	DIYPSGSSTINYNEKFKS
D08	PELVRPQGASVKLSCASGYIFT	SYWMH	WVKQRPQGQLEWIG	EINPNSGGTINYNEKFKS
E07	AELVRPQGASVKLSCASGYIFT	SYEWH	WVKQTPVHGLEWIG	AIDPETGTTAYNQKFKG
G08	PELVRPQGASVKLSCASGYIFT	DYIIN	WVKQRPQGQLEWIG	WIYPSGSNTINYNEKFKG
G10	AELVRPQGASVKLSCASGYIFT	SYWMH	WVKQRPQGQLEWIG	RIHPSDSTDNYNQKFKG
25G09	AELVRPQGASVKLSCASGYIFT	TYPIE	WVKQNHAKSLEWIG	NFHPYNDDTINYNEKFKG
F04	TELVRPQGASVKLSCASGYIFT	SYWMH	WVKQRPQGQLEWIG	NINPNSGGTINYNQKFKG
H02	AELVRPQGASVKLSCASGYIFT	SYWMH	WVKQRPQGQLEWIG	NIDPSDSETINYNQKFKG
H01	AELVMPGASVKLSCASGYIFT	SYWMH	WVKQRPQGQLEWIG	EIDPSDSYTINYN*KG
25C05	PELVRPGTYSVKMSCKASGYFFF	NYWMK	WVTPQGQGLEWIG	QIFPASGSIIYYNEMHKD
B01	AELVRPQGASVKMSCKASGYIFT	SYWIT	WVKQRPQGQLEWIG	DIYPSGSSTINYNEKFKS
B05	AELVRPQGSSVKLSCDKSYFAFM	RHAMH	WVKQRPQHGLEWIG	SFTMYSDATEYSENFKG
B11	AELVRPQGASVKMSCKASGYIFT	SYWIT	WVKQRPQGQLEWIG	DIYPSGSSTINYNEKFKS

KABAT III A

25G05	GGLVQAGNSLSSLSCAASGFTFS	DYMS	WVRQPPGKALEWLG	FIRNKANGYTTTEYASVKG
C10	GGLVQPGGSSLSSLSCAASGFTFS	DYMMN	WVRQPPGKALEWLW	LIRHKANGYTTMEYASVKG
B07	GGLVQPGGSSLSSLSCAASGFTFS	DYMS	WVRQPPGKALEWLW	LIRNKANGYTTTEYASVKG

KABAT III B

G05	GGLVKPGGSSLKLSCAASGFTFS	DYGMH	WVRQAPKEGLEWVA	YISSSSSTIYADTVKG
B12	GGLVQPGESLKLSCNEYEPF	SDHMS	WVR*****VA	AINSDDGSSYYPDTRMER
D04	GGLVQPGGSSLRLSCAASGFTFS	SYAMS	WVA*APGKGLEWVS	AISGSGGTTYYADSVKG
D05	GGLVQPGGSSLRLSCAASGFTFS	SYAMS	WVA*APGKGLEWVS	AISGSGGTTYYADSVKG
F12	GGLVQPGESWKLSCVITQO***	***	WVRQ*PERKLELVA	AISDGGTTYYPDTRMER
F06	GGLVQPGGSSLRLSCAASGFTFS	SYAMS	WVA*APGKGLEWVS	AISGSGGTTYYADSAKG
D02	GGLVQPGESLKLSCSENEYIP	*DMS	WVRQDSGE*LELVA	AISDGGTTYYPDTRMER
F09	GDLVQPGGSSLKLSCAASGFTFS	SYGMS	WVRQTPDKRLEWA	TISSGGSYTYPDPSVKG

KABAT III C

E06	GGLVQPGGSMKLSCAASGFTFS	DAWMD	WVRQSPEKGLEWVA	EIRNKANNHATYYAESVKG
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KABAT V A

C04	AELVPKPGASVKLSCASGYIFT	EYTIH	WVKQRSQQGLEWIG	WFYPGSGSIKYNEKFKD
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FIG. 10a



ER-3

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CDR-3

RISITROTSKNQFFLKLKNLNSVTTEDTATYYCAR
 PISITRETSKNQFFLQLNLSVTTEDTATYYCAG
 RISITROTSKNQFFLQLNLSVTTEDTATYYCAR
 RISITROTSKNQFFLKLKNLNSVTTEDTATYYCAR

EGNWWDGFAY
 DRDKLGPWFAF
 DSSGSMDF
 VSSGYESMDY

RLSISKDTSKSQVFLKMNSLQLDDTAVYYCAK	HGDSSGYFDY	
RLSISKDTSKSQVFFKMNSLQLADDTAIYYCAR	NDGYY	
RLSISKDTSKSQVFLKMNSLQLDDTAMYYCAK	LGRGYAMDY	
RLSISKDTSKSQVFFKMNSLQLADDTAIYYCAR	KRDYDYDRGYYYAMDY	
RLSISKDTSKSQVFLKMNSLQLDDTAMYYCAK	YDGSSFFAY	
RLSISKDTSKSQVFLKMNSLQLDDTARYCAY	EGYYFFAY	
RLSISKDTSKSQVFLKMNSLQLDDTARYCAY	IYDGSSDYYAMDY	
RLSISKDTSKSQVFLKMNSLQLDDTAMYYCAR	13 nt.	Ps.gene/Unproductiv
RLSISKDTSKSQVFLKMNSLQLDDTAMYYCAR	21 nt.	Unproductive
RLSISKDTSKSQVFFKMNSLQLADDTAIYYCAR	28 nt.	Unproductive
RLSISKDTSKSQVFFKMNSLQLDDTAMYYCAK	37 nt.	Unproductive
RLSISKDTSKSQVFLKMNSLQLDDTAMYYCAY	32 nt.	Unproductive

KATMTVDKSSSTAYMELARLTSEDSAVYYCAR	40 nt.	Unproductive
KATMTVDKSSSTAYMELARLTSEDSAVYYCAR	22 nt.	Unproductive

KATLTVDKSSSTAYMQLSSLTSEDSAVYYCVR	RGLTYAMDY	
KATLTVDTSSTAYMQLSSLTSEDSAVYYCAR	YSSNYFDY	
KATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR	PWDHYYYGMDV	
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCTL	LYYYAMDY	
KATLTVDTSSTAYMQLSSLTSEDSAVYYCAR	SSGYDY	
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR	GAARATNAY	
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR	GGFAY	
KATLTVDTSSTAYMQLSSLTSEDSAVYYCAR	SPMDY	
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAI	EVPGGFYATDY	
KATLTVKSSSTVYELSLRSLTSEDSAVYYCAR	MDYYGSSLWFAY	
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR	TTVVAFDY	
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR	KRDYSTXFDH	
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR	TGTEFAY	Ps.gene
KAAWAVDTSSSTAYMQLSSLTSEDSTAVYYFCL*	24 nt.	Ps.gene/Unproductiv
KATLTVDKPSSTAYMQLSSLTSEDASAYYYCAR	9 nt.	Unproductive
KATLTANTSSSTAYMELSSLTSEDSAVYYCAR	23 nt.	Unproductive
KATLTVDTSSTSYMQLSSLTSEDSAVYYCAR	15 nt.	Unproductive

RFTISRDNSQSILYLQMNALRAEDSATYYCAR	YMILOGAMDY	
RFTISRDNSQSILYLQMNALRAEDSATYYCAR	GIYYDGSSYAMDY	
RFTISRDNSQSILYLQMNALRAEDSATYYCAR	23 nt.	Unproductive

RFTISRDNAKNTLFLQMTSLRSEDTAMYYCAR	AKFHLYFDY	
RFTISRDNTKTKTLYLQMSLRSEDTAYYYCAR	REGIVESRLDGDV	Ps.gene
RFTISRDNSKNTLYLQMNLSLRAEDTAYYYCAD	RGLHWFDP	Ps.gene
RFTISRDNSKNTLYLQMNLSLRAEDTAYYYCAR	RNYGSSPFDY	Ps.gene
RFTISRDNSKNTLYLQMNLSLRAEDTAYYYCAR	PRMPPSFY	Ps.gene
RFTISRDNSKNTLYLQMNLSLRAEDTAYYYCAR	43 nt.	Ps.gene/Unproductiv
RFTISRDNTKTKTLYLQMSLRSEDTALYYCAR	28 nt.	Ps.gene/Unproductiv
RFTISRDNAKNTLYLQMNLSLKSEDTAMYYCAR	35 nt.	Unproductive

RFTISRDDSKSRVYLQMNSLRAEDTGIYYCTG	30 nt.	Unproductive
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KATLTADKSSSTVYELSLRSLTSEDSAVYFCAR HEDRDSGGYAMDY

FIG. 10 b



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CDR 2

FRAMEWORK 3

CDR 3

KABAT HUMAN VD1

HAQKFQG	STSTAYMELRSLRSEDATAVYCAR	GEGWDHFQY
GYAOKFQG	RVTIRRKSTSTAYMELLSSRLSEDATAVYCAR	GSRYGYDCSGYYYL
	RVTMTRNTSISTATMELLSSRLSEDATAVYCAR	LAHESGSPVWFEDR

KABAT HUMAN VH2

KHQLQPSLKS	RTVISVDTSKNQFSLKLSSVTAADTAVYYCAR	GGVVPAAIMDV
KS	RTVISVDTSKNQFSLKLSSVTAADTAVYYCAR	MARYYDFWSGYSAYYD
SLKS	RLSISQDTSRNQFSRLSSVTAADTAVYYCAR	HRNWGSQPVHFDY
	ESTSTAYMELSSRLSEDATVYYCAR	DSYGDYYGHHY

KABAT HUMAN VD3

ISYITSSSYTYADSVKG	RFTISRDNNAKNSLYLQMNNSLRADDTAVYYCAR	DRGFGTYSPSPDY
SVKG	RFTISRDDSKSIAILQVNNSLKTEDTAVYYCTR	TIYYDSSGYFW
YADSVKG	RFTISRDNNAKNSLYLQMNNSLRADDTAVYYCAR	GIALDAFDI
YYADSVKG	RFTISRDNNSKNTLYLQMNNSLRADDTAVYYCAR	53 11. UNPROD REARR
DSVKG	RFTISRDNNAKNSLYLQMNNSLRADDTAVYYCAR	DHSGTGGGGSYSF
VSAISGSGGTTYYADSVKG	RFTISRDNPKNTLYLQMNNSLRADDTAVYYCAR	KDNLWFDP
AVISYDGNSKYYADSVKG	RFTISRDNNSKNTLYLQMNNSLRADDTAVYYCAR	DILGRRGVVVVPPGGRSIIYGGMDV
GAVISYDGNSKYYADSVKG	RFTISRDNNSKNTLYLQMNNSLRADDTAVYYCAS	LEGIGTIYYGMDV
QYASVKG	AKNSLYLQMNNSLRADDTAVYYCVR	DDSSSWPKHFQH
		SGVYVLDY

KNOWN FAMILY

AVYYCAR DPRIAARPDYVVYMDV
TAMYYCAR GAEVVEPTARYYYGLNV

FIG. 11



FR1	CDR1	FR2
Y TFT	SY GIS	W V T T G P W T R D L R W M G
GEKPGSSVKVSKCASKASGYTFT	D Y F M N	W M R Q A P G Q R L E W M G
Q V Q L Q E I G P R T G E A S E T L S L C I A V S G D S I S	S G N W * I	W V R Q P P G K G L E W I G
Q V Q L Q E S G P G L V K * S E T L S L T C T V S G G S I S	S Y W S	W I r q p p G K G L E W I G
Y G T F T	N Y C M H	W V R Q D H A Q G L E W M G
Q V Q L Q E S G P G L V K p S E T L S L Y C A V S G D S I S	S G N W * I	W V R Q P P G K G L E W I G
G P R L G E A S E T L S L T C T V S G G S I S	S S S Y W	W I R Q P P G K G L E W I G
Q V Q L Q E S G P G L V K p S E T L S L T C T V S G G S I S	S Y Y W S	W I R Q P P G K G L E W I G
L S L I C A V S G G S I S	S G N W * I	W V R Q P P G K G L E W I G
S E T L S L T C A V Y G G S F S	G Y W S	W I R Q P P G K G L E W I G
Q V Q L V Q S G A E V K K P G A S V K V S C A K S G Y T F T	N Y C M H	W V R Q V L A Q Q G L E W M G
S E T L S L I C A V S G D S I S	S G N W * I	W V R Q P P G K G L E W I G
S R A Q T G E A S E T L S L T C T V S G G S I S	S S S Y W G	W I R Q P P G K G L E W I G
C P L T C T V S G G S V S G S	Y Y W S	W I R Q P P G K G L E W I G
G L V K P S E T L S L T C T V S G G S I S	S Y Y W S	W I G S P p G K G L E W I G
S F E T L S L I C A V S G D S I S	S G N W * I	W V R Q P P G K G L E W I G
Q V Q L V Q S G A E V K K P G S V V S C A K S G G T F S	S V A I S	W V R Q A P G Q G L E W M G
Q V Q L Q O W G A G L L K E S E T L S L T C A V Y G G S F S	G Y W S	W I R Q P P G K G L E W I G
Q L Q L Q E S G P G L V K P S E T L S L T C T V S G G S I S	S S S Y W G	W I R Q P P G K G L E W I G
G P G L V K P S Q T L S L T C T V S G G S I S	S G G Y W S	W I R Q N P G K G L E W I G

* indicates stop codon (unsure as sequence remains in frame)
 • sequence terminates due to internal restriction site
 lower case denotes frame shift

CDR2	FR3	CDR3
W I S A Y N G N T N Y A Q K L Q G	R V I M T T D T S T S T A Y M E L R S L R S D D T A V Y Y C A R	D T V S S
W I N A G N G N T K Y S Q K L Q G	R V T I T R D T S A T S T A Y M Q L S S R S E D T A V Y Y C A R	D T V S S
E I H H S G S T Y Y N P S L K S	R I T M S V D T S K N Q F Y L K L S S *	
R I Y T S G S T N Y N P S L K S	R V T I S V D T S K N Q F S L K L S S *	D T V S S
L V C P S D G S T S Y A Q K F Q A	R V T I T R D T S M S T A Y M E L S S R S E D T A V Y Y C A R	D T V S S
E I H H S G S T Y Y N P S L K S	R I T M S V D T S K N Q F Y L K L S S *	D T V S S
E I N H S G S T N Y N P S L K S	R V T I S V D T S K N Q F S L K L S S *	D T V S S
Y I Y S G S T N Y N P S L K S	R V T I S V D T S K N Q F S L K L S S *	D T V S S
E I H H S G S T Y Y N P S L K S	R I T M S V D T S K N Q F Y L K L S S *	D T V S S
E I N H S G S T N Y N P S L K S	R V T I S V D T S K N Q F S L K L S S *	D T V S S
E I N H S G S T N Y N P S L K S	R I T M S V D T S K N Q F Y L K L S S *	D T V S S
E I N H S G S T N Y N P S L K S	R V T I T R D T S M S T A Y M E L S S R S E D T A V Y Y C A R	D T V S S
E I N H S G S T N Y N P S L K S	R I T M S V D T S K N Q F Y L K L S S *	D T V S S
S I Y Y S G S T Y Y N P S L K S	R V T I P V D T S K N Q F S L K L S S *	D T V S S
Y I Y S G S T N Y N P S L K S	R V T I S V D T S K N Q F S L K L S S *	D T V S S
R I Y T S G S T N Y N P S L K S	R V T M S V D T S K N Q F S L K L S S *	D T V S S
E I H H S G S T Y Y N P S L K S	R I T M S V D T S K N Q F Y L K L S S *	D T V S S
R I I P I L G I A N Y A Q K F Q G	R V T I T A D K S T S T A Y M E L S L R S E D T A V Y Y C A R	D T V S
E I N H S G S T N Y N P S L K S	R V T I S V D T S K N Q F S L K L S S *	D T V S
E I N H S G S T N Y N P S L K S	R V T I S V D T S K N Q F S L K L S S *	D T V S
Y I Y S G S T Y Y N P S L K S	R V T I S V D T S K N Q F S L K L S S *	D T V S S

FIG. 12



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pSW1

HindIII site AAGCTT

M K Y L L P T A A
GCATGCAAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCAACAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCTGGTGGCGCCTCACAGAGCCTGTCCATCACATGCCACCGTCTCAGGTTG
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGGCTATGGTGAAACTGGGTTGCCAGCCTCCAGGAAAGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGGTGATGGAAACACAGACTATAATTCACTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACACTCAAGAGCCAAGTTCTAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTGTGCCAGAGAGAGATTAGGCTTGACTIONGGGC
370 380 390 400 410 420

Q G T T V T V S S SmaI
CAAGGCACACGGTCACCGTCTCCTCATAATAAGAGCTATCCCAGGCTAACGCTCGAATTG
430 440 450 460 470 480

FIG. 13



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pSW2

HindIII AAGCTT

M K Y L L P T A A
GCATGCAAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCAACCGCGATGCCAGGTGCAGCTGCAGGAGTC
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGGCTATGGTGTAAACTGGGTCGCCAGCCTCCAGGAAGGGTCTGGAGTGC
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTGGGGTGTGGAAACACAGACTATAATTAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTCTTAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTAGGCTTGACTACTGGGC
370 380 390 400 410 420

Q G T T V T V S S
CAAGGCACCACGGTCACCGTCTCTCATAATAAGAGCTCGAATTGCCAACGCTGCATGC
430 440 450 460 470 480

M K Y L L P T A A A G
AAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCCTACGGCAGCCGCTGG
490 500 510 520 530 540

L L L L A A Q P A M A D I V L T Q S P A
TTGTTATTACTCGCTGCCAACCGCGATGCCAGCATCGTCTGACTCAGTCTCCAGCC
550 560 570 580 590 600

S L S A S V G E T V T I T C R A S G N I
TCCCTTCTCGCTGTGGAGAAACTGTCACCATCACATGCGACCAAGGGAAATT
610 620 630 640 650 660

H N Y L A W Y Q Q K Q G K S P Q L L V Y
CACAATTATTAGCATGGTATCAGCAGAAACAGGGAAATCTCCTCAGCTCTGGTCTAT
670 680 690 700 710 720

FIG. 14a



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Y T T T L A D G V P S R F S G S G S G T
TATACAAACACCTTAGCAGATGGTGTGCCATCAAGGTCAGTGGCAGTGGATCAGGAACA
730 740 750 760 770 780

Q Y S L K I N S L Q P E D F G S Y Y C Q
CATATATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTTGGGAGTTATTACTGTCAA
790 800 810 820 830 840

H F W S T P R T F G G G T K L E I K R
CATTTTGGAGTACTCCTCGGACGTTGGAGGCACCAAGCTGAAATCAAACGGTAA
850 860 870 880 890 900

TAAGAGCTCGAATTC
910

FIG. 14 b

pSW1HPOLYMYC

HindIII site AAGCTT

M K Y L L P T A A
GCATGCAAATTCATTTCAAGGGAGACAGTCATAATGAAATACCTATTGCCAACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q
GCTGGATTGTTATTACTCGCTGCCAACAGCGATGGCCAGGTGCAGCTGCAG
70 80 90 100 110 PstI

Polylinker
TCTAGA GTCGAC CTCGAG
XbaI SalI XhoI

MYC PEPTIDE
V T V S S E Q K L I S E E D L N * *
GGTCACCGTCTCTCAGAACAAAAACTCATCTCAGAAGAGGATCTGAATTAATAA
BstEII

GGGCTAAGCTCGAATTC

FIG. 15



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1		CDR1	49
VH3	QVQLQESGPVELVKPGASVKMSCKASGYTFT	SYVMH	WVKQKPGAGLEWIG
VE8	QVQLQESGPVELVKPGASVKMSCKASGYTFT	SYVMH	WVKQKPGQGLEWIG
VH-D1.3	QVQLKESGPGLVAPSQSLSITCTVSGFSLT	GYGVN	WVRQPPGKGLEWLG
50	CDR2		94
VH3	YINPYNDGTYNEKFKG	KATLTS	KATLTS
VE8	YINPYNDGSKYNEKFKG	KSSNTAYMELSSLTSED	SSNTAYMELSSLTSED
VH-D1.3	MIW GGDGNTDYNALKS	SAVYYCAV	SAVYYCAR
95	CDR3	113	
VH3	LLLRYFFDY	WGQGTTVTVSS	
VE8	GAVVSYAMYD	WGQGTTVTVSS	
VH-D1.3	ERDYRLDY	WGQGTTLTVSS	

FIG. 16

FR1	QVQLQESGGGLVQPGGSLRLSCAASGFTFS	
	SYAMS	CDR1
FR2	WVRQAPGKGLEWVS	
	AISGGSGTYYADSVKG	CDR2
FR3	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAM	
	WRGIATPVSFDLGYFDY	CDR3

FIG. 17



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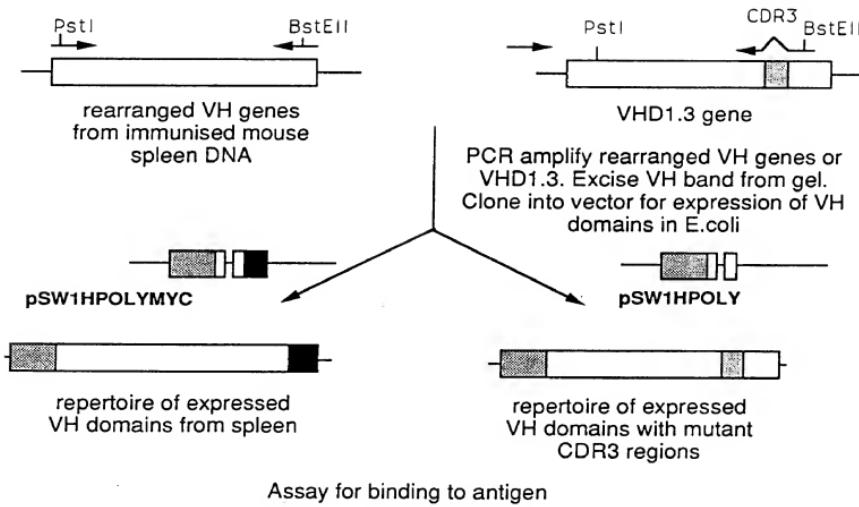


FIG. 18



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pSW2HPOLY

HindIII AAGCTT

			M	K	Y	L	L	P	T	A	A
GCATGCAAATTCTATTCAAGGAGACAGTCATAATGAAATACTATTGCCCTACGGCAGCC	10	20	30	40	50	60					

A	G	L	L	L	A	A	Q	P	A	M	A	Q	V	Q	L	Q
GCTGGATTGTTATTACTCGCTGCCAACCGAGCGATGGCCAGGTGCAGCTGCAG	70	80	90	100	110											

TCTAGA GTCGAC CTCGAG
XbaI SalI XhoI

V	T	V	S	S												
GGTCACCGTCTCCTCATATAAGAGCTCGAATTGCCAAGCTTGCATGC	430	440	450	460	470	480										

M	K	Y	L	L	P	T	A	A	A	G
AAATTCTATTCAAGGAGACAGTCATAATGAAATACTATTGCCCTACGGCAGCCGCTGGA	490	500	510	520	530	540				

L	L	L	A	A	Q	P	A	M	A	D	I	V	L	T	Q	S	P	A
TTGTTATTACTCGCTGCCAACCGAGCGATGGCCGACATCGTCTGACTCAGTCTCCAGGC	550	560	570	580	590	600												

S	L	S	A	S	V	G	E	T	V	T	I	I	T	C	R	A	S	G	N	I
TCCCTTCTCGCTCTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGAAATTATT	610	620	630	640	650	660														

H	N	Y	L	A	W	Y	Q	Q	K	Q	G	K	S	P	Q	L	L	V	Y
CACAATTATTAGCATGGTATCAGCAGAACAGGGAAATCCCTCAGCTCTGGTCTA	670	680	690	700	710	720													

Y	T	T	L	A	D	G	V	P	S	R	F	S	G	S	G	S	G	T
TATACAACAAACCTTAGCATGGTGTGCCATCAAGGTTAGTGGCAGTGGATCAGGAACAA	730	740	750	760	770	780												

Q	Y	S	L	K	I	N	S	L	Q	P	E	D	F	G	S	Y	Y	C	Q
CAATATTCCTCAAGATCAACAGCTGCCAACCTGAAGATTGGAGTTACTGTCAA	790	800	810	820	830	840													

H	F	W	S	T	P	R	T	F	G	G	G	T	K	L	E	I	K	R
CATTTTGGAGTACTCTCGACGTTGGCTGGAGGCCAACAGCTGGAAATCAAACCGTAA	850	860	870	880	890	900												

TAAGAGCTCGAATT
910

FIG. 19



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	M	K	Y	L	L	P	T
AAGCTTGATGCAAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACG	10	20	30	40	50	60	
GCAGCCGCTGGATTGTTAATCTCGCTGCCAACAGCGATGGCCAGGTGAGCTGCAG	70	80	90	100	110	120	
GCAGCCGCTGGATTGTTAATCTCGCTGCCAACAGCGATGGCCAGGTGAGCTGCAG	130	140	150	160	170	180	
GGTCAGGACCTGGCTGGCCCTCACAGAGCTGTCATCACATGACCGCTCA	190	200	210	220	230	240	
GGTCAGGACCTGGCTGGCCCTCACAGAGCTGTCATCACATGACCGCTCA	250	260	270	280	290	300	
GGTCAGGACCTGGCTGGCCCTCACAGAGCTGTCATCACATGACCGCTCA	310	320	330	340	350	360	
GGTCAGGACCTGGCTGGCCCTCACAGAGCTGTCATCACATGACCGCTCA	370	380	390	400	410	420	
GGTCAGGACCTGGCTGGCCCTCACAGAGCTGTCATCACATGACCGCTCA	430	440	450	460	470	480	
GGTCAGGACCTGGCTGGCCCTCACAGAGCTGTCATCACATGACCGCTCA	490	500	510	520	530	540	
GGTCAGGACCTGGCTGGCCCTCACAGAGCTGTCATCACATGACCGCTCA	550	560	570	580	590	600	
GGTCAGGACCTGGCTGGCCCTCACAGAGCTGTCATCACATGACCGCTCA	610	620	630	640	650	660	
GGTCAGGACCTGGCTGGCCCTCACAGAGCTGTCATCACATGACCGCTCA	670	680	690	700	710	720	
GGTCAGGACCTGGCTGGCCCTCACAGAGCTGTCATCACATGACCGCTCA	730	740	750	760	770	780	
GGTCAGGACCTGGCTGGCCCTCACAGAGCTGTCATCACATGACCGCTCA	790	800	810	820	830	840	
TAATAAGAGCTC	850						

FIG. 20



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	M	K	Y	L	L	P	T	A	A
GCATGCAAATTCTATTCAGGAGACAGTCATAATGAAATACCTATTGCCACGGCAGCC	10	20	30	40	50	50	60		
A G L L L A A Q P A M A Q V Q L Q E S									
GCTGGATTGTTATTACTCGCTGCCAACAGCGATGGCCAGGTGCGACTGCAGGAGTC	70	80	90	100	110	110	120		
G P G L V A P S Q S L S I T C T V S G F									
GGACCTGGCTGGTGGCCCTCACAGACCTGTCATCACATGCCACGGTCTCAGGGTTC	130	140	150	160	170	170	180		
S L T G Y G V N W V R Q P P G K G L E W									
TCATTAACCGGCTATGGTGTAACTGGGTTGCCAGCCTCAGGAAAGGGTCTGGAGTGG	190	200	210	220	230	230	240		
L G M I W G D G N T D Y N S A L K S R L									
CTGGGAATGATTGGGTGATGGAAACAGACACTATAATTAGCTCTCAAATCCAGACTG	250	260	270	280	290	290	300		
S I S K D N S K S Q V F L K M N S L H T									
AGCATCAGCAAGGACAACCTCAAAGGCCAAGTTCTAAATGAAACAGTCTGCACACT	310	320	330	340	350	350	360		
D D T A R Y Y C A R E R D Y R L D Y W G									
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTAGGCTTGACTACTGGGC	370	380	390	400	410	410	420		
Q G T T V T V S S R T P E M P V L E N R									
CAAGGCACACGGTCACCGTCTCCTCACGGACACAGAAATGCCCTGTTCTGGAAAACGG	430	440	450	460	470	470	480		
A A Q G D I T A P G G A R R L T G D O T									
GCTGCTCAGGGCAGTATTACTGCACCCGGCGGTGCTGCCGTTAACGGGTGATCAGACT	490	500	510	520	530	530	540		
A A L R D S L S D K P A K N I I L L I G									
GCGCTCTGCGTGAATTCTAGCGATAAACCTGCAAAAATATTATGGCTGATTGGC	550	560	570	580	590	590	600		
D G M G D S E I T A A R N Y A E G A G G									
GATGGGATGGGGACTCGGAATTACTGCCACGTAATTATGCCAAGGTGCGGGCGGC	610	620	630	640	650	650	660		
F F K G I D A L P L T G Q Y T H Y A L N									
TTTTTTAAAGGTATAGATGCCCTACCGCTAACGGGCAATACACTCACTATGCCGCTGAAT	670	680	690	700	710	710	720		
K K T G K P D Y V T D S A A S A T A W S									
AAAAAAACCGCAAACCGGACTACGTCACCGACTCGCTGCATCAGCAACCGCTGCTCA	730	740	750	760	770	770	780		

FIG. 21a



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T G V K T Y N G A L G V D I H E K D H P
ACCGGTGCAAAACCTATAACGGCGCCTGGCGCTGATATTACGAAAAAGATCACCA
790 800 810 820 830 840

T I L E M A K A A G L A T G N V S T A E
ACGATTCTGAAATGGAAAAGCCGCAGGTCTGGCGACCGTAACGTTCTACCCGAGAG
850 860 870 880 890 900

L Q D A T P A A L V A H V T S R K C Y G
TTGAGGATGCCACGCCGCTGGCTGGCACATGTCACCTCGCAAATGCTACGGT
910 920 930 940 950 960

P S A T S E K C P G N A L E K G G K G S
CCGAGCGCACCAGTGGAAAATGTCGGTAACGCTGGAAAAAGCGGAAAGGATCG
970 980 990 1000 1010 1020

I T E Q L L N A R A D V T L G G G A K T
ATTACCGAACAGCTGTTAACGCTCGTGGCAGCTTACGCTGGCGGGCGCAAACACC
1030 1040 1050 1060 1070 1080

F A E T A T A G E W Q G K T L R E Q A Q
TTTGCTGAAACGCCAACCGCTGGTGAATGGCAGGGAAAACGCTGGCTGAACAGGCACAG
1090 1100 1110 1120 1130 1140

A R G Y Q L V S D A A S L N S V T E A N
GCGCGTGGTTACAGTGGTGAGCGATGCTGCCTCACTGAATTGGTACGGAAGCGAAT
1150 1160 1170 1180 1190 1200

Q Q K P L L G L F A D G N M P V R W L G
CAGCAAAACCCCTGCTTGGCTGGCTGACGGCAATATGCCAGTGGCTGGTAGGA
1210 1220 1230 1240 1250 1260

P K A T Y H G N I D K P A V T C T P N P
CCGAAAGCAACGTACCATGGCAATATCGATAAGCCCGAGTCACCTGTACGCCAAATCCG
1270 1280 1290 1300 1310 1320

Q R N D S V P T L A Q M T D K A I E L L
CAACGTAATGACAGTGTACCAACCCCTGGCGCAGATGACCGACAAAGCATTGAATTGTTG
1330 1340 1350 1360 1370 1380

S K N E K G F F L Q V E G A S I D K Q D
AGTAAAAATGAGAAAGGCTTTTCCCTGCAAGTGAAGGTGCGTCAATCGATAAACAGGAT
1390 1400 1410 1420 1430 1440

H A A N P C G Q I G E T V D L D E A V Q
CATGCTGCGAATCCTGGCAATTGGCGAGACGGTGCATCGATGAAGCCGTACAA
1450 1460 1470 1480 1490 1500

R A L E F A K K E G N T L V I V T A D H
CGGGCGCTGGAATCGCTAAAAGGAGGGTAAACACGCTGGTCATAGTCACCGCTGATCAC
1510 1520 1530 1540 1550 1560



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A H A S Q I V A P D T K A P G L T Q A L
GCCCCACGCCAGCCAGATTGTTGCCGGATACCAAAGCTCCGGGCCTCACCCAGGCCTA
1570 1580 1590 1600 1610 1620

N T K D G A V M V M S Y G N S E E D S Q
AATACCAAAGATGGCCAGTCAGTGATGGTGTACGGGAACCTCGAAGAGGATTCAACAA
1630 1640 1650 1660 1670 1680

E H T G S Q L R I A A Y G P H A A N V V
GAACATACCGGCAGTCAGTTGCCGTATTGCCGGTATGCCCGCATGCCGCAATGTTGTT
1690 1700 1710 1720 1730 1740

G L T D Q T D L F Y T M K A A L G L K *
GGACTGACCGACCCAGACCGATCTCTTCTACACCATGAAAGCCGCTCTGGGCTGAAATAA
1750 1760 1770 1780 1790 1800

AACCGCGCCGGAGTGAATTTCGCTGCCGGGTGGTTTTGCTGTTAGC
1810 1820 1830 1840 1850

FIG. 21c



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M K Y L L P T A A
GCATGCAAATTCTATTCAGGAGACAGTCATAATGAAATACCTATTGCCAACGGCAGCC
10 20 30 40 50 60

A G L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCAACAGCGATGCCAGGTGCGACTGCAGGAGTC
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCATCACATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACGGCTATGGTGTAAACTGGGTCGCCAGCCTCAGGAAAGGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTGGGTGATGAAACAGACTATAATTAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCGAACAGGACAACCTCCAAGAGGCCAAGTTCTAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTAGGCTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S * *
CAAGGCACACGGTCACCGTCTCTCATATAAGAGCTATCCCGGGAGCTTGCATGCAA
430 440 450 460 470 480

M K Y L L P T A A A G L
TTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCAACGGCAGCCGCTGGATTG
490 500 510 520 530 540

L L L A A Q P A M A D I E L V D L E I K
TTATTAATCGCTGCCAACAGCGATGCCAGCTCGAGCTCGACCTCGAGATCAA
550 560 570 580 590 600

R E Q K L I S E E D L N * *
CGGGAAACAAAAACTCATCTCAGAAGAGGATCTGAATTAATAATGATCAAACGGTAATAAG
610 620 630 640 650 660

GATCCAGCTCGAATTC
670

FIG. 22



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A

Q V Q L Q E S G P G L V Q P S Q S L S I
CAGGTGCAGCTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCATC

10 20 30 40 50 60

T C T V S G F S L T S Y G V H W V R Q S
ACCTGCACAGTCTCTGTTCTCATTAACTAGCTATGGTGTACACTGGGTCGCCAGTCT
C

70 80 90 100 110 120

P G K G L E W L G M I W G D G N T D Y N
CCAGGAAGGGCTGGAGTGGCTGGAAATGATTTGGGTGATGGAACACAGACTATAAT
130 140 150 160 170 180

S A L K S R L S I S K D N S K S Q V F L
TCAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACCTCAAGAGCCAAGTTCTTA
190 200 210 220 230 240

K M N S L H T D D T A R Y Y C A R E R D
AAAATGAAACAGTCTGCACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAT
250 260 270 280 290 300

Y R L D Y W G Q G T T V T V S S
TATAGGCTTGAACAGTCTGGGCAAGGGACACGGTCACCGTCTCCTCA
310 320 330 340

FIG. 23